

Sequence Listing PCT-JP03-00117.txt
SEQUENCE LISTING

<110> Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tame

<120> Method of monitoring gene expression

<130> 4439-4023

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<150> JP P2002-002396

<151> 2002-01-09

<160> 14

<170> PatentIn Ver. 2.1

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Gly Ser Tyr Ile Asn Tyr Glu Gly Leu Lys Lys Phe Leu Lys Glu Asp	
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agc gtg aag gat gga agt aac gat aag aaa gca cgc tgg gac gat tca	144
Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser	
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gat gaa tcc aag ttt gtg gaa gag ttg gat aag gaa ctt gaa aaa gtc	192
Asp Glu Ser Lys Phe Val Glu Glu Leu Asp Lys Glu Leu Glu Lys Val	
50 55 60	
tat ggt ttt caa cta aaa aag tac aat aac ttg atg gag aga ttg tcc	240
Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser	
65 70 75 80	
cat ctg gag aaa caa aca gat acg gaa gca gcc ata aag gcc ttg gac	288
His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp	
85 90 95	
gct gat gca ttc caa cgt gta ttg gag gaa ctg tta agc gag tct acc	336
Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr	
100 105 110	
gaa tta gac aat ttt aag aga ttg aac ttt act ggg ttt gct aag att	384
Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile	
115 120 125	
gtt aag aaa cat gac aag cta tat cca aag tat cca tct gtt aaa tct	432
Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser	
130 135 140	

Sequence Listing PCT-JP03-00117.txt

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Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser	
165 170 175	
aat ttt aac act gca tct gaa ccc tta gcc agc gct tct aag ttt tct	576
Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser	
180 185 190	
agc att gtc agc aat gac ata gac atg aat ttc aga agc ttt aaa ttt	624
Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe	
195 200 205	
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Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg	
210 215 220	
cat ctt ccc gtg ttg gtc tac gcc aat gtt ccc tcc gaa aac gat gac	720
His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp	
225 230 235 240	
ctg gtc aat aga ttc gaa tca gat ata tca aat aat gat gaa att gtg	768
Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val	
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260 265 270	
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275 280 285	
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Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu	
290 295 300	
aga tta agg tgg act ggc cag tta tct gat aag ccg gat att ttc ttg	960
Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu	
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325 330 335	
gat cta act aaa ttg caa ttg aaa caa aaa ttc att aac ggg ttt att	1056
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Sequence Listing PCT-JP03-00117.txt

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Arg Thr Val Tyr Thr	Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys						
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Ile Arg Val Thr Ile	Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser						
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Phe Asp Arg Glu Arg	Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr						
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Glu Tyr Ala Lys Phe	Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser						
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Ser Leu Asp Ser Ser	Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys						
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Sequence Listing PCT-JP03-00117.txt

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Sequence Listing PCT-JP03-00117.txt

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 100 105 110
 Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile
 115 120 125
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 130 135 140
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 Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser
 180 185 190
 Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe
 195 200 205
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 225 230 235 240
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Sequence Listing PCT-JP03-00117.txt

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580 585 590

Ala Val Pro Val Ser Gln Glu Glu Asn Glu Arg Ile Thr Ser Gln Gly
595 600 605

Asp Leu Glu Ala Asp Gly Ser Ser Asp Glu Glu Thr Glu Gln Glu Pro
610 615 620

His Ser Lys Arg Ser Lys Lys Val Arg Arg Arg Lys Pro Lys Ala Thr
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Phe Leu Arg Ile Leu Ala Gly Arg Asp Pro Lys Leu Met Gly Val Asp
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Sequence Listing PCT-JP03-00117.txt															
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Ile	Ile	Gln 755	Gln	Arg	Ser	Gly	Gln 760	His	Leu	Asp	Ala	Pro 765	Leu	Gly	Pro
Val	Leu 770	Val	Ser	Ile	Val	Leu 775	Phe	Val	Thr	Leu	Val 780	Val	Asn	Phe	Val
Met 785	Ala	Phe	Arg	Asn	Ala 790	Ala	Lys	Ser	Arg	Gln 795	Glu	Leu	Gln	Ile	Gln 800
Asn	Leu	Glu	Val	Pro 805	Glu	Arg	Ile	Pro	Glu 810	Val	Leu	Arg	Pro	Leu 815	Gln
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gaa tct gat ttt gtg gag gcc ttg gat aaa gaa cta gaa aag gtt tac Glu Ser Asp Phe Val Glu Ala Leu Asp Lys Glu Leu Lys Val Tyr	192
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tta gag gaa aac act aaa tca gct gaa aaa atc caa aaa ata aat tct Leu Glu Glu Asn Thr Lys Ser Ala Glu Lys Ile Gln Lys Ile Asn Ser	288
gag cag ttc aaa aac acc tta gaa gaa tgt cta gat gag gct caa aga Glu Gln Phe Lys Asn Thr Leu Glu Glu Cys Leu Asp Glu Ala Gln Arg	336
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Sequence Listing PCT-JP03-00117.txt

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432			
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ttg Leu	aaa Lys 150	gaa Glu	ctt Leu
cct Pro	ttc Phe	aac Asn 155	aat Asn
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tat Tyr 165	agg Arg	atc Ile	tca Ser
tat Tyr	ctg Leu 170	tac Tyr	gag Glu
ttc Phe	ttg Leu 175	aga Arg	tca Ser
528			
aat Asn	tat Tyr	gat Asp	cat His 180
cca Pro	aat Asn	acg Thr	gtg Val
tct Ser 185	aaa Lys	tca Ser	tta Leu
gca Ala	agt Ser 190	act Thr	tct Ser
576			
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ttt Phe	tct Ser	aac Asn	ctt Leu 200
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624			
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cat His	gat Asp	gat Asp 215	aat Asn
ata Ile	atg Met	gag Glu	gtt Val 220
aag Lys	gct Ala	aga Arg	atc Ile
672			
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tat Tyr	gcg Ala	tcg Ser 235	gtt Val
cca Pro	aat Asn	gaa Glu	aat Asn 240
720			
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tca Ser	gat Asp 250	gtc Val	cgc Arg
gta Val	caa Gln	cct Pro 255	gaa Glu
768			
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816			
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ata Ile			
1008			
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act Thr	ggt Gly 350	aat Asn	tca Ser
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Sequence Listing PCT-JP03-00117.txt

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caa Gln	agt Ser	att Ile 435	aga Arg	gtc Val	act Thr	atc Ile	gat Asp 440	tcc Ser	aat Asn	atc Ile	atg Met	tac Tyr 445	att Ile	aga Arg	gag Glu	1344
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cgt Arg 465	gac Asp	gat Asp	att Ile	gat Asp	tcc Ser 470	aat Asn	att Ile	ccc Pro	aac Asn	cca Pro 475	ttg Leu	agg Arg	ttt Phe	tta Leu	aga Arg 480	1440
gca Ala	gga Gly	gaa Glu	tat Tyr	tcg Ser 485	aag Lys	ttc Phe	ccc Pro	tat Tyr	tct Ser 490	gta Val	atg Met	gag Glu	att Ile	aag Lys 495	gtt Val	1488
ata Ile	aac Asn	caa Gln	gat Asp 500	aat Asn	tct Ser	caa Gln	atg Met	cct Pro 505	aat Asn	tat Tyr	gag Glu	tgg Trp	att Ile 510	aaa Lys	gat Asp	1536
tta Leu	act Thr	aat Asn 515	tca Ser	cat His	tta Leu	gtt Val	aac Asn 520	gaa Glu	gtt Val	cca Pro	aaa Lys	ttt Phe 525	tct Ser	ttg Leu	tac Tyr	1584
ttg Leu 530	caa Gln	ggg Gly	gtg Val	gct Ala	tca Ser	ctg Leu 535	ttt Phe	ggg Gly	gaa Glu	gac Asp	gat Asp 540	aaa Lys	tat Tyr	gtc Val	aac Asn	1632
att Ile 545	ttg Leu	cca Pro	ttc Phe	tgg Trp	ttg Leu 550	ccc Pro	gat Asp	tta Leu	gaa Glu	acc Thr 555	gac Asp	atc Ile	aga Arg	aag Lys	aac Asn 560	1680
cct Pro	cag Gln	gag Glu	gct Ala	tac Tyr 565	gaa Glu	gaa Glu	gag Glu	aag Lys	aaa Lys 570	act Thr	tta Leu	caa Gln	aaa Lys	caa Gln 575	aag Lys	1728
agc Ser	att Ile	cat His	gat Asp 580	aaa Lys	ctt Leu	gat Asp	aat Asn	atg Met 585	aga Arg	agg Arg	tta Leu	tcc Ser	aaa Lys 590	atc Ile	tct Ser	1776
gta Val	cca Pro	gat Asp 595	gga Gly	aag Lys	acc Thr	act Thr	gaa Glu 600	aga Arg	caa Gln	ggg Gly	caa Gln	aaa Lys 605	gat Asp	cag Gln	aat Asn	1824
act Thr 610	cgc Arg	cac His	gtt Val	att Ile	gca Ala	gat Asp 615	tta Leu	gaa Glu	gat Asp	cac His	gaa Glu 620	tca Ser	tca Ser	gat Asp	gaa Glu	1872

Sequence Listing PCT-JP03-00117.txt

gaa ggt act gca ttg ccc aag aaa tct gca gtc aaa aaa ggg aag aaa Glu Gly Thr Ala Leu Pro Lys Lys Ser Ala Val Lys Lys Gly Lys Lys 625 630 635 640	1920
ttc aaa acg aat gca gct ttc ttg aaa att ctt gct gga aaa aat att Phe Lys Thr Asn Ala Ala Phe Leu Lys Ile Leu Ala Gly Lys Asn Ile 645 650 655	1968
tca gaa aat gga aat gat cca tac tcc gac gat aca gac agt gcc tct Ser Glu Asn Gly Asn Asp Pro Tyr Ser Asp Asp Thr Asp Ser Ala Ser 660 665 670	2016
tct ttc caa tta cct ccg gga gtt aaa aaa cca gtt cac ctt ttg aaa Ser Phe Gln Leu Pro Pro Gly Val Lys Lys Pro Val His Leu Leu Lys 675 680 685	2064
aat gcc ggt cct gtc aaa gtt gag gca aaa gtt tgg ctc gcc aat gaa Asn Ala Gly Pro Val Lys Val Glu Ala Lys Val Trp Leu Ala Asn Glu 690 695 700	2112
cgt aca ttc aat aga tgg tta agt gta acc aca ttg ctg agt gta ttg Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Thr Leu Leu Ser Val Leu 705 710 715 720	2160
acc ttt tct atc tat aat tca gtg caa aaa gcc gaa ttt cca caa cta Thr Phe Ser Ile Tyr Asn Ser Val Gln Lys Ala Glu Phe Pro Gln Leu 725 730 735	2208
gct gat ctg ttg gcc tat gta tat ttc ttt ttg act ttg ttt tgc gga Ala Asp Leu Leu Ala Tyr Val Tyr Phe Phe Leu Thr Leu Phe Cys Gly 740 745 750	2256
gta tgg gct tat aga acc tac tta aaa aga tta act ctt att aaa ggt Val Trp Ala Tyr Arg Thr Tyr Leu Lys Arg Leu Thr Leu Ile Lys Gly 755 760 765	2304
aga agt ggt aag cat ttg gat gca cct gtg gga cct att ttg gtt gca Arg Ser Gly Lys His Leu Asp Ala Pro Val Gly Pro Ile Leu Val Ala 770 775 780	2352
gtt gta tta atc gtt acc ttg gtt gtt aac ttt agt gtg gct ttt aaa Val Val Leu Ile Val Thr Leu Val Val Asn Phe Ser Val Ala Phe Lys 785 790 795 800	2400
gag gcc gct agg agg gaa aga gga tta gta aac gtt tcc tcc cag cct Glu Ala Ala Arg Arg Glu Arg Gly Leu Val Asn Val Ser Ser Gln Pro 805 810 815	2448
tcg tta ccc cgt aca cta aaa cca att caa gat ttt atc ttc aat ttg Ser Leu Pro Arg Thr Leu Lys Pro Ile Gln Asp Phe Ile Phe Asn Leu 820 825 830	2496
gtt ggg gaa taa Val Gly Glu 835	2508

<210> 4
 <211> 835
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 <400> 4

Sequence Listing PCT-JP03-00117.txt

Met Leu Phe Gly Ile Lys Leu Ala Asn Asp Val Tyr Pro Pro Trp Lys
 1 5 10 15
 Asp Ser Tyr Ile Asp Tyr Glu Arg Leu Lys Lys Leu Leu Lys Glu Ser
 20 25 30
 Val Ile His Asp Gly Arg Ser Ser Val Asp Ser Trp Ser Glu Arg Asn
 35 40 45
 Glu Ser Asp Phe Val Glu Ala Leu Asp Lys Glu Leu Glu Lys Val Tyr
 50 55 60
 Thr Phe Gln Ile Ser Lys Tyr Asn Ala Val Leu Arg Lys Leu Asp Asp
 65 70 75 80
 Leu Glu Glu Asn Thr Lys Ser Ala Glu Lys Ile Gln Lys Ile Asn Ser
 85 90 95
 Glu Gln Phe Lys Asn Thr Leu Glu Glu Cys Leu Asp Glu Ala Gln Arg
 100 105 110
 Leu Asp Asn Phe Asp Arg Leu Asn Phe Thr Gly Phe Ile Lys Ile Val
 115 120 125
 Lys Lys His Asp Lys Leu His Pro Asn Tyr Pro Ser Val Lys Ser Leu
 130 135 140
 Leu Gln Val Arg Leu Lys Glu Leu Pro Phe Asn Asn Ser Glu Glu Tyr
 145 150 155 160
 Ser Pro Leu Leu Tyr Arg Ile Ser Tyr Leu Tyr Glu Phe Leu Arg Ser
 165 170 175
 Asn Tyr Asp His Pro Asn Thr Val Ser Lys Ser Leu Ala Ser Thr Ser
 180 185 190
 Lys Leu Ser His Phe Ser Asn Leu Glu Asp Ala Ser Phe Lys Ser Tyr
 195 200 205
 Lys Phe Trp Val His Asp Asp Asn Ile Met Glu Val Lys Ala Arg Ile
 210 215 220
 Leu Arg His Leu Pro Ala Leu Val Tyr Ala Ser Val Pro Asn Glu Asn
 225 230 235 240
 Asp Asp Phe Val Asp Asn Leu Glu Ser Asp Val Arg Val Gln Pro Glu
 245 250 255
 Ala Arg Leu Asn Ile Gly Ser Lys Ser Asn Ser Leu Ser Ser Asp Gly
 260 265 270
 Asn Ser Asn Gln Asp Val Glu Ile Gly Lys Ser Lys Ser Val Ile Phe
 275 280 285
 Pro Gln Ser Tyr Asp Pro Thr Ile Thr Thr Leu Tyr Phe Asp Asn Asp
 290 295 300
 Phe Phe Asp Leu Tyr Asn Asn Arg Leu Leu Lys Ile Ser Gly Ala Pro
 305 310 315 320
 Thr Leu Arg Leu Arg Trp Ile Gly Lys Leu Leu Asp Lys Pro Asp Ile
 325 330 335

Sequence Listing PCT-JP03-00117.txt

Phe Leu Glu Lys Arg Thr Phe Thr Glu Asn Thr Glu Thr Gly Asn Ser
 340 345 350
 Ser Phe Glu Glu Ile Arg Leu Gln Met Lys Ala Lys Phe Ile Asn Asn
 355 360 365
 Phe Ile Phe Lys Asn Asp Pro Ser Tyr Lys Asn Tyr Leu Ile Asn Gln
 370 375 380
 Leu Arg Glu Arg Gly Thr Gln Lys Glu Glu Leu Glu Lys Leu Ser Arg
 385 390 395 400
 Asp Phe Asp Asn Ile Gln Asn Phe Ile Val Glu Glu Lys Leu Gln Pro
 405 410 415
 Val Leu Arg Ala Thr Tyr Asn Arg Thr Ala Phe Gln Ile Pro Gly Asp
 420 425 430
 Gln Ser Ile Arg Val Thr Ile Asp Ser Asn Ile Met Tyr Ile Arg Glu
 435 440 445
 Asp Ser Leu Asp Lys Asn Arg Pro Ile Arg Asn Pro Glu Asn Trp His
 450 455 460
 Arg Asp Asp Ile Asp Ser Asn Ile Pro Asn Pro Leu Arg Phe Leu Arg
 465 470 475 480
 Ala Gly Glu Tyr Ser Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val
 485 490 495
 Ile Asn Gln Asp Asn Ser Gln Met Pro Asn Tyr Glu Trp Ile Lys Asp
 500 505 510
 Leu Thr Asn Ser His Leu Val Asn Glu Val Pro Lys Phe Ser Leu Tyr
 515 520 525
 Leu Gln Gly Val Ala Ser Leu Phe Gly Glu Asp Asp Lys Tyr Val Asn
 530 535 540
 Ile Leu Pro Phe Trp Leu Pro Asp Leu Glu Thr Asp Ile Arg Lys Asn
 545 550 555 560
 Pro Gln Glu Ala Tyr Glu Glu Glu Lys Lys Thr Leu Gln Lys Gln Lys
 565 570 575
 Ser Ile His Asp Lys Leu Asp Asn Met Arg Arg Leu Ser Lys Ile Ser
 580 585 590
 Val Pro Asp Gly Lys Thr Thr Glu Arg Gln Gly Gln Lys Asp Gln Asn
 595 600 605
 Thr Arg His Val Ile Ala Asp Leu Glu Asp His Glu Ser Ser Asp Glu
 610 615 620
 Glu Gly Thr Ala Leu Pro Lys Lys Ser Ala Val Lys Lys Gly Lys Lys
 625 630 635 640
 Phe Lys Thr Asn Ala Ala Phe Leu Lys Ile Leu Ala Gly Lys Asn Ile
 645 650 655
 Ser Glu Asn Gly Asn Asp Pro Tyr Ser Asp Asp Thr Asp Ser Ala Ser
 660 665 670

Sequence Listing PCT-JP03-00117.txt

Ser Phe Gln Leu Pro Pro Gly Val Lys Lys Pro Val His Leu Leu Lys
675 680 685

Asn Ala Gly Pro Val Lys Val Glu Ala Lys Val Trp Leu Ala Asn Glu
690 695 700

Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Thr Leu Leu Ser Val Leu
705 710 715 720

Thr Phe Ser Ile Tyr Asn Ser Val Gln Lys Ala Glu Phe Pro Gln Leu
725 730 735

Ala Asp Leu Leu Ala Tyr Val Tyr Phe Phe Leu Thr Leu Phe Cys Gly
740 745 750

Val Trp Ala Tyr Arg Thr Tyr Leu Lys Arg Leu Thr Leu Ile Lys Gly
755 760 765

Arg Ser Gly Lys His Leu Asp Ala Pro Val Gly Pro Ile Leu Val Ala
770 775 780

Val Val Leu Ile Val Thr Leu Val Val Asn Phe Ser Val Ala Phe Lys
785 790 795 800

Glu Ala Ala Arg Arg Glu Arg Gly Leu Val Asn Val Ser Ser Gln Pro
805 810 815

Ser Leu Pro Arg Thr Leu Lys Pro Ile Gln Asp Phe Ile Phe Asn Leu
820 825 830

Val Gly Glu
835

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<211> 1947
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(1944)

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Met Lys Phe Gly Glu His Leu Ser Lys Ser Leu Ile Arg Gln Tyr Ser
1 5 10 15

tac tat tat att agt tat gat gat ctg aag act gag cta gaa gat aac 96
Tyr Tyr Tyr Ile Ser Tyr Asp Asp Leu Lys Thr Glu Leu Glu Asp Asn
20 25 30

tta tct aag aat aac ggt cag tgg acg caa gaa ttg gaa aca gat ttt 144
Leu Ser Lys Asn Asn Gly Gln Trp Thr Gln Glu Leu Glu Thr Asp Phe
35 40 45

tta gaa tct ttg gag atc gag tta gac aag gtt tac aca ttt tgc aaa 192
Leu Glu Ser Leu Glu Ile Glu Leu Asp Lys Val Tyr Thr Phe Cys Lys
50 55 60

gtt aag cat agt gaa gtt ttt aga cgt gta aaa gag gtt caa gaa caa 240
Val Lys His Ser Glu Val Phe Arg Arg Val Lys Glu Val Gln Glu Gln

Sequence Listing PCT-JP03-00117.txt

65	70	75	80													
gtg Val	caa Gln	cat His	act Thr	ggt Val 85	cgt Arg	ttg Leu	tta Leu	gac Asp	tcc Ser 90	aat Asn	aat Asn	cct Pro	cct Pro	act Thr 95	cag Gln	288
cta Leu	gat Asp	ttt Phe	gag Glu 100	att Ile	cta Leu	gaa Glu	gaa Glu 105	gaa Glu 105	cta Leu	agt Ser	gat Asp	atc Ile	att Ile 110	gcc Ala	gat Asp	336
ggt Val	cat His	gat Asp 115	cta Leu	gca Ala	aag Lys	ttt Phe	tcg Ser 120	aga Arg	cta Leu	aac Asn	tac Tyr	act Thr 125	ggg Gly	ttc Phe	caa Gln	384
aag Lys	att Ile 130	atc Ile	aag Lys	aaa Lys	cac His	gat Asp 135	aag Lys	aag Lys	aca Thr	ggg Gly	ttt Phe 140	atc Ile	ttg Leu	aaa Lys	cca Pro	432
ggt Val 145	ttc Phe	caa Gln	ggt Val	aga Arg	tta Leu 150	gac Asp	tct Ser	aaa Lys	cca Pro	ttt Phe 155	ttc Phe	aag Lys	gaa Glu	aac Asn	tat Tyr 160	480
gac Asp	gaa Glu	cta Leu	gtc Val 165	ggt Val 165	aaa Lys	att Ile	tcc Ser	caa Gln	cta Leu 170	tat Tyr	gat Asp	att Ile	gcc Ala	aga Arg 175	act Thr	528
tca Ser	ggg Gly	cgc Arg	cca Pro 180	atc Ile	aag Lys	gga Gly	gac Asp	tca Ser 185	tct Ser	gct Ala	ggg Gly	ggg Gly 190	aag Lys 190	caa Gln	caa Gln	576
aat Asn	ttc Phe 195	ggt Val	aga Arg	cag Gln	aca Thr	aca Thr	aag Lys 200	tat Tyr	tgg Trp	ggt Val	cac His	cct Pro 205	gat Asp	aac Asn	att Ile	624
aca Thr 210	gaa Glu	ttg Leu	aag Lys	ctg Leu	atc Ile	atc Ile 215	ttg Leu	aag Lys	cat His	tta Leu	cca Pro 220	gtg Val	tta Leu	gtc Val	ttc Phe	672
aac Asn 225	act Thr	aat Asn	aag Lys	gaa Glu	ttc Phe 230	gaa Glu	aga Arg	gaa Glu	gat Asp	tcc Ser 235	gct Ala	att Ile	act Thr	tcg Ser	atc Ile 240	720
tat Tyr	ttt Phe	gat Asp	aat Asn	gaa Glu 245	aat Asn	cta Leu	gac Asp	ctt Leu	tat Tyr 250	tat Tyr	ggc Gly	aga Arg	tta Leu	aga Arg 255	aaa Lys	768
gat Asp	gaa Glu	ggg Gly	gca Ala 260	gaa Glu	gcc Ala	cac His	aga Arg	ttg Leu 265	aga Arg	tgg Trp	tat Tyr	ggg Gly	ggg Gly 270	atg Met	tct Ser	816
aca Thr	gac Asp	acg Thr 275	atc Ile	ttt Phe	gta Val	gaa Glu	aga Arg 280	aag Lys	acc Thr	cat His	aga Arg	gag Glu 285	gat Asp	tgg Trp	act Thr	864
ggg Gly 290	gag Glu	aaa Lys	tct Ser	gtc Val	aag Lys	gca Ala 295	aga Arg	ttt Phe	gcg Ala	cta Leu	aag Lys 300	gaa Glu	cgt Arg	cat His	gtt Val	912
aat Asn 305	gac Asp	ttc Phe	tta Leu	aag Lys	ggg Gly 310	aaa Lys	tat Tyr	act Thr	gtt Val	gat Asp 315	caa Gln	gta Val	ttt Phe	gcc Ala	aag Lys 320	960
atg	cgt	aaa	gaa	ggc	aag	aag	cca	atg	aac	gaa	att	gaa	aac	ttg	gag	1008

Sequence Listing PCT-JP03-00117.txt

Met	Arg	Lys	Glu	Gly 325	Lys	Lys	Pro	Met	Asn 330	Glu	Ile	Glu	Asn	Leu 335	Glu		
gcg	tta	gca	tcc	gaa	att	caa	tac	gtc	atg	tta	aag	aaa	aag	ttg	aga	1056	
Ala	Leu	Ala	Ser 340	Glu	Ile	Gln	Tyr	Val 345	Met	Leu	Lys	Lys	Lys 350	Leu	Arg		
cct	gta	gtg	aga	tca	ttc	tac	aat	aga	act	gct	ttt	caa	tta	cct	ggt	1104	
Pro	Val	Val 355	Arg	Ser	Phe	Tyr	Asn 360	Arg	Thr	Ala	Phe	Gln 365	Leu	Pro	Gly		
gat	gca	aga	gtt	cgt	atc	tcc	ctt	gat	aca	gag	tta	act	atg	gtg	aga	1152	
Asp	Ala	Arg	Val	Arg	Ile	Ser 375	Leu	Asp	Thr	Glu	Leu 380	Thr	Met	Val	Arg		
gaa	gac	aac	ttt	gat	ggg	gtg	gat	aga	act	cat	aag	aat	tgg	agg	aga	1200	
Glu	Asp	Asn	Phe	Asp	Gly 390	Val	Asp	Arg	Thr	His 395	Lys	Asn	Trp	Arg	Arg 400		
act	gat	att	ggg	gtc	gat	tgg	cca	ttc	aag	cag	cta	gat	gac	aag	gat	1248	
Thr	Asp	Ile	Gly	Val 405	Asp	Trp	Pro	Phe	Lys 410	Gln	Leu	Asp	Asp	Lys 415	Asp		
att	tgc	cgt	ttc	cca	tat	gca	gtc	ctg	gaa	gtt	aaa	ttg	caa	act	caa	1296	
Ile	Cys	Arg	Phe 420	Pro	Tyr	Ala	Val	Leu 425	Glu	Val	Lys	Leu	Gln 430	Thr	Gln		
cta	ggg	caa	gaa	cct	cca	gag	tgg	gta	cgt	gaa	tta	gtc	ggg	tct	cac	1344	
Leu	Gly	Gln 435	Glu	Pro	Pro	Glu	Trp 440	Val	Arg	Glu	Leu	Val 445	Gly	Ser	His		
tta	gtt	gag	cca	gtc	cca	aaa	ttc	tcc	aag	ttt	att	cat	ggg	gtg	gct	1392	
Leu	Val 450	Glu	Pro	Val	Pro	Lys 455	Phe	Ser	Lys	Phe	Ile 460	His	Gly	Val	Ala		
acc	tta	cta	aat	gat	aaa	gtg	gat	tca	atc	cca	ttt	tgg	tta	cct	caa	1440	
Thr	Leu	Leu	Asn	Asp	Lys 470	Val	Asp	Ser	Ile	Pro 475	Phe	Trp	Leu	Pro	Gln 480		
atg	gat	gtt	gat	atc	agg	aaa	cct	cca	cta	cca	aca	aat	att	gaa	ata	1488	
Met	Asp	Val	Asp	Ile 485	Arg	Lys	Pro	Pro	Leu 490	Pro	Thr	Asn	Ile	Glu 495	Ile		
aca	aga	ccc	ggg	aga	tcc	gat	aac	gaa	gat	aac	gac	ttc	gat	gag	gat	1536	
Thr	Arg	Pro	Gly 500	Arg	Ser	Asp	Asn	Glu 505	Asp	Asn	Asp	Phe	Asp 510	Glu	Asp		
gat	gag	gat	gac	gct	gct	ttg	gtt	gct	gcc	atg	aca	aac	gca	ccc	ggg	1584	
Asp	Glu	Asp 515	Asp	Ala	Ala	Leu	Val 520	Ala	Ala	Met	Thr	Asn 525	Ala	Pro	Gly		
aat	tct	ctt	gat	ata	gaa	gaa	tct	gtt	ggg	tac	ggg	gct	act	tcg	gcc	1632	
Asn	Ser 530	Leu	Asp	Ile	Glu	Glu 535	Ser	Val	Gly	Tyr	Gly 540	Ala	Thr	Ser	Ala		
ccc	acc	tcc	aac	act	aat	cat	gtt	gtt	gag	agt	gct	aat	gct	gct	tat	1680	
Pro	Thr	Ser	Asn	Thr	Asn 550	His	Val	Val	Glu	Ser 555	Ala	Asn	Ala	Ala	Tyr 560		
tat	caa	aga	aag	atc	agg	aat	gcc	gaa	aat	cct	atc	tcc	aag	aaa	tac	1728	
Tyr	Gln	Arg	Lys	Ile 565	Arg	Asn	Ala	Glu	Asn 570	Pro	Ile	Ser	Lys	Lys 575	Tyr		

Sequence Listing PCT-JP03-00117.txt

tat gaa atc gtg gca ttt ttt gac cac tat ttt aac ggt gat caa ata	1776
Tyr Glu Ile Val Ala Phe Phe Asp His Tyr Phe Asn Gly Asp Gln Ile	
580	585
tct aaa atc cca aaa ggt act act ttt gat act caa att cgt gcc cca	1824
Ser Lys Ile Pro Lys Gly Thr Thr Phe Asp Thr Gln Ile Arg Ala Pro	
595	600
ccg gaa aga cga tat gtg tgc cag ttc gtg tgg aac caa aag ttt act	1872
Pro Glu Arg Arg Tyr Val Cys Gln Phe Val Trp Asn Gln Lys Phe Thr	
610	620
ttg cca ctg aaa gaa cct acc tgt ctt ggt tgt cca tct cga tat tgt	1920
Leu Pro Leu Lys Glu Pro Thr Cys Leu Gly Cys Pro Ser Arg Tyr Cys	
625	630
635	640
tggtg gctg gtg tct cca cta ctt tat taa	1947
Trp Ala Val Ser Pro Leu Leu Tyr	
645	

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<211> 648

<212> PRT

<213> Saccharomyces cerevisiae

<400> 6

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30	
Leu Ser Lys Asn Asn Gly Gln Trp Thr Gln Glu Leu Glu Thr Asp Phe	
35	40
45	
Leu Glu Ser Leu Glu Ile Glu Leu Asp Lys Val Tyr Thr Phe Cys Lys	
50	55
60	
Val Lys His Ser Glu Val Phe Arg Arg Val Lys Glu Val Gln Glu Gln	
65	70
75	80
Val Gln His Thr Val Arg Leu Leu Asp Ser Asn Asn Pro Pro Thr Gln	
85	90
95	
Leu Asp Phe Glu Ile Leu Glu Glu Glu Leu Ser Asp Ile Ile Ala Asp	
100	105
110	
Val His Asp Leu Ala Lys Phe Ser Arg Leu Asn Tyr Thr Gly Phe Gln	
115	120
125	
Lys Ile Ile Lys Lys His Asp Lys Lys Thr Gly Phe Ile Leu Lys Pro	
130	135
140	
Val Phe Gln Val Arg Leu Asp Ser Lys Pro Phe Phe Lys Glu Asn Tyr	
145	150
155	160
Asp Glu Leu Val Val Lys Ile Ser Gln Leu Tyr Asp Ile Ala Arg Thr	
165	170
175	
Ser Gly Arg Pro Ile Lys Gly Asp Ser Ser Ala Gly Gly Lys Gln Gln	
180	185
190	

Sequence Listing PCT-JP03-00117.txt

Asn Phe Val Arg Gln Thr Thr Lys Tyr Trp Val His Pro Asp Asn Ile
 195 200 205
 Thr Glu Leu Lys Leu Ile Ile Leu Lys His Leu Pro Val Leu Val Phe
 210 215
 Asn Thr Asn Lys Glu Phe Glu Arg Glu Asp Ser Ala Ile Thr Ser Ile
 225 230 235 240
 Tyr Phe Asp Asn Glu Asn Leu Asp Leu Tyr Tyr Gly Arg Leu Arg Lys
 245 250 255
 Asp Glu Gly Ala Glu Ala His Arg Leu Arg Trp Tyr Gly Gly Met Ser
 260 265 270
 Thr Asp Thr Ile Phe Val Glu Arg Lys Thr His Arg Glu Asp Trp Thr
 275 280 285
 Gly Glu Lys Ser Val Lys Ala Arg Phe Ala Leu Lys Glu Arg His Val
 290 295 300
 Asn Asp Phe Leu Lys Gly Lys Tyr Thr Val Asp Gln Val Phe Ala Lys
 305 310 315 320
 Met Arg Lys Glu Gly Lys Lys Pro Met Asn Glu Ile Glu Asn Leu Glu
 325 330 335
 Ala Leu Ala Ser Glu Ile Gln Tyr Val Met Leu Lys Lys Lys Leu Arg
 340 345 350
 Pro Val Val Arg Ser Phe Tyr Asn Arg Thr Ala Phe Gln Leu Pro Gly
 355 360 365
 Asp Ala Arg Val Arg Ile Ser Leu Asp Thr Glu Leu Thr Met Val Arg
 370 375 380
 Glu Asp Asn Phe Asp Gly Val Asp Arg Thr His Lys Asn Trp Arg Arg
 385 390 395 400
 Thr Asp Ile Gly Val Asp Trp Pro Phe Lys Gln Leu Asp Asp Lys Asp
 405 410 415
 Ile Cys Arg Phe Pro Tyr Ala Val Leu Glu Val Lys Leu Gln Thr Gln
 420 425 430
 Leu Gly Gln Glu Pro Pro Glu Trp Val Arg Glu Leu Val Gly Ser His
 435 440 445
 Leu Val Glu Pro Val Pro Lys Phe Ser Lys Phe Ile His Gly Val Ala
 450 455 460
 Thr Leu Leu Asn Asp Lys Val Asp Ser Ile Pro Phe Trp Leu Pro Gln
 465 470 475 480
 Met Asp Val Asp Ile Arg Lys Pro Pro Leu Pro Thr Asn Ile Glu Ile
 485 490 495
 Thr Arg Pro Gly Arg Ser Asp Asn Glu Asp Asn Asp Phe Asp Glu Asp
 500 505 510
 Asp Glu Asp Asp Ala Ala Leu Val Ala Ala Met Thr Asn Ala Pro Gly
 515 520 525

Sequence Listing PCT-JP03-00117.txt

Asn Ser Leu Asp Ile Glu Glu Ser Val Gly Tyr Gly Ala Thr Ser Ala
 530 535 540

Pro Thr Ser Asn Thr Asn His Val Val Glu Ser Ala Asn Ala Ala Tyr
 545 550 555 560

Tyr Gln Arg Lys Ile Arg Asn Ala Glu Asn Pro Ile Ser Lys Lys Tyr
 565 570 575

Tyr Glu Ile Val Ala Phe Phe Asp His Tyr Phe Asn Gly Asp Gln Ile
 580 585 590

Ser Lys Ile Pro Lys Gly Thr Thr Phe Asp Thr Gln Ile Arg Ala Pro
 595 600 605

Pro Glu Arg Arg Tyr Val Cys Gln Phe Val Trp Asn Gln Lys Phe Thr
 610 615 620

Leu Pro Leu Lys Glu Pro Thr Cys Leu Gly Cys Pro Ser Arg Tyr Cys
 625 630 635 640

Trp Ala Val Ser Pro Leu Leu Tyr
 645

<210> 7
 <211> 390
 <212> DNA
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<220>
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 <222> (1)..(387)

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 1 5 10 15

ttg ccc aca cga gtt gag cca aaa gtg ttc ttt gcc aat gag cgt acc 96
 Leu Pro Thr Arg Val Glu Pro Lys Val Phe Phe Ala Asn Glu Arg Thr
 20 25 30

ttt ttg tcg tgg ttg aac ttt aca gtt atg ctg gga ggc ctt ggt gta 144
 Phe Leu Ser Trp Leu Asn Phe Thr Val Met Leu Gly Gly Leu Gly Val
 35 40 45

ggt tta ctg aat ttt ggt gac aag ata ggt agg gtc agt gca gga cta 192
 Gly Leu Leu Asn Phe Gly Asp Lys Ile Gly Arg Val Ser Ala Gly Leu
 50 55 60

ttt act ttt gtt gcc atg ggt aca atg ata tac gcg ctt gta aca tac 240
 Phe Thr Phe Val Ala Met Gly Thr Met Ile Tyr Ala Leu Val Thr Tyr
 65 70 75 80

cac tgg aga gct gct gcg att aga cgt aga gga tca ggt cct tat gat 288
 His Trp Arg Ala Ala Ala Ile Arg Arg Arg Gly Ser Gly Pro Tyr Asp
 85 90 95

gac aga ttg ggg ccc act ttg ttg tgc ttt ttc tta ttg gtt gct gtc 336
 Asp Arg Leu Gly Pro Thr Leu Leu Cys Phe Phe Leu Leu Val Ala Val
 100 105 110

Sequence Listing PCT-JP03-00117.txt

att atc aac ttt ata tta aga ttg aag tac aat gac gct aac act aag 384
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115 120 125

tta tga 390
Leu

<210> 8
<211> 129
<212> PRT
<213> Saccharomyces cerevisiae

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35 40 45
Gly Leu Leu Asn Phe Gly Asp Lys Ile Gly Arg Val Ser Ala Gly Leu
50 55 60
Phe Thr Phe Val Ala Met Gly Thr Met Ile Tyr Ala Leu Val Thr Tyr
65 70 75 80
His Trp Arg Ala Ala Ile Arg Arg Arg Gly Ser Gly Pro Tyr Asp
85 90 95
Asp Arg Leu Gly Pro Thr Leu Leu Cys Phe Phe Leu Leu Val Ala Val
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Leu

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<213> Saccharomyces cerevisiae

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Pro Lys Lys Lys Ser Leu Ile Ala Ile Leu Ser Thr Cys Val Leu Phe
20 25 30
ttc ctc gtg ttt ata att ggt gct aaa ttt caa tat gtt tcc gtt ttc 144
Page 19

Sequence Listing PCT-JP03-00117.txt

Phe	Leu	Val	Phe	Ile	Ile	Gly	Ala	Lys	Phe	Gln	Tyr	Val	Ser	Val	Phe		
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Ser	Lys	Phe	Leu	Asp	Asp	Arg	Gly	Asp	Asn	Glu	Ser	Leu	Gln	Leu	Leu		
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Asn	Asp	Ile	Glu	Phe	Thr	Arg	Leu	Gly	Leu	Thr	Pro	Arg	Glu	Pro	Val		
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Ile	Ile	Lys	Asp	Val	Lys	Thr	Gly	Lys	Glu	Arg	Lys	Leu	His	Gly	Arg		
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Phe	Leu	His	Ile	Thr	Asp	Ile	His	Pro	Asp	Pro	Tyr	Tyr	Val	Glu	Gly		
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Ser	Ser	Ile	Asp	Ala	Val	Cys	His	Thr	Gly	Lys	Pro	Ser	Lys	Lys	Lys		
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Val	Ile	Leu	Met	Glu	Glu	Thr	Leu	Arg	Trp	Ile	Lys	Glu	Asn	Leu	Arg		
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Asp	Lys	Ile	Asp	Phe	Val	Ile	Trp	Thr	Gly	Asp	Asn	Ile	Arg	His	Asp		
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Asn	Asp	Arg	Lys	His	Pro	Arg	Thr	Glu	Ala	Gln	Ile	Phe	Asp	Met	Asn		
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Asn	Ile	Val	Ala	Asp	Lys	Met	Thr	Glu	Leu	Phe	Ser	Ala	Gly	Asn	Glu		
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gaa	gat	cca	aga	gat	ttt	gat	gtg	tct	gtc	att	cca	agt	ctt	gga	aac	672	
Glu	Asp	Pro	Arg	Asp	Phe	Asp	Val	Ser	Val	Ile	Pro	Ser	Leu	Gly	Asn		
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act	aga	gaa	tat	tat	agg	att	tgg	aaa	aat	ttt	gtt	ccg	cag	cag	cag	768	
Thr	Arg	Glu	Tyr	Tyr	Arg	Ile	Trp	Lys	Asn	Phe	Val	Pro	Gln	Gln	Gln		
				245					250					255			
caa	aga	act	ttt	gat	agg	agt	gct	tca	ttt	ttg	act	gaa	gtt	att	cca	816	
Gln	Arg	Thr	Phe	Asp	Arg	Ser	Ala	Ser	Phe	Leu	Thr	Glu	Val	Ile	Pro		
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ggg	aag	ctt	gct	gtc	ctg	tca	att	aac	acg	ctg	tac	tta	ttc	aag	gcc	864	
Gly	Lys	Leu	Ala	Val	Leu	Ser	Ile	Asn	Thr	Leu	Tyr	Leu	Phe	Lys	Ala		
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Sequence Listing PCT-JP03-00117.txt

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Leu	Leu	Leu	Trp	Phe	Gly	Tyr	Val	Leu	Glu	Glu	Leu	Arg	Ser	Arg	Gly	
	305				310					315					320	
atg	aaa	gta	tgg	tta	agt	gga	cat	gta	cct	cca	atc	gca	aaa	aat	ttc	1008
Met	Lys	Val	Trp	Leu	Ser	Gly	His	Val	Pro	Pro	Ile	Ala	Lys	Asn	Phe	
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Asp	Gln	Ser	Cys	Tyr	Asp	Lys	Phe	Thr	Leu	Trp	Thr	His	Glu	Tyr	Arg	
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Asp	Ile	Ile	Ile	Gly	Gly	Leu	Tyr	Gly	His	Met	Asn	Ile	Asp	His	Phe	
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atc	cca	acg	gat	ggt	aaa	aaa	gct	aga	aaa	tcg	tta	ttg	aaa	gcc	atg	1152
Ile	Pro	Thr	Asp	Gly	Lys	Lys	Ala	Arg	Lys	Ser	Leu	Leu	Lys	Ala	Met	
	370					375					380					
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	385				390					395					400	
gaa	gaa	act	gaa	ttg	aat	aga	att	ctg	gat	cac	gct	atg	gcg	gca	aaa	1248
Glu	Glu	Thr	Glu	Leu	Asn	Arg	Ile	Leu	Asp	His	Ala	Met	Ala	Ala	Lys	
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Glu	Val	Phe	Leu	Met	Gly	Ala	Lys	Pro	Ser	Asn	Lys	Glu	Ala	Tyr	Met	
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Arg	Val	Asp	Glu	Lys	Asn	Val	Glu	Asn	Glu	Lys	Lys	Lys	Lys	Glu	Lys	
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Lys	Asp	Lys	Lys	Lys	Lys	Lys	Pro	Ile	Thr	Arg	Lys	Glu	Leu	Ile	Glu	
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cgc	tat	tcc	att	gtg	aac	ata	ggt	ggt	tca	gtc	att	cca	act	ttc	aat	1488
Arg	Tyr	Ser	Ile	Val	Asn	Ile	Gly	Gly	Ser	Val	Ile	Pro	Thr	Phe	Asn	
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Pro	Ser	Phe	Arg	Ile	Trp	Glu	Tyr	Asn	Ile	Thr	Asp	Ile	Val	Asn	Asp	
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tcc	aat	ttt	gca	gtt	tcg	gag	tat	aag	ccc	tgg	gat	gaa	ttt	ttc	gag	1584
Ser	Asn	Phe	Ala	Val	Ser	Glu	Tyr	Lys	Pro	Trp	Asp	Glu	Phe	Phe	Glu	
		515					520					525				
tca	cta	aat	aag	att	atg	gaa	gac	tct	ttg	cta	gaa	gat	gaa	atg	gac	1632
Ser	Leu	Asn	Lys	Ile	Met	Glu	Asp	Ser	Leu	Leu	Glu	Asp	Glu	Met	Asp	
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Sequence Listing PCT-JP03-00117.txt

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aaa aac aag aag aaa aag aaa aat gac aag act atg cca att gag atg	1728
Lys Asn Lys Lys Lys Lys Lys Asn Asp Lys Thr Met Pro Ile Glu Met	
565 570 575	
cca gac aaa tac gaa ctc ggc cct gca tat gta ccg cag tta ttc act	1776
Pro Asp Lys Tyr Glu Leu Gly Pro Ala Tyr Val Pro Gln Leu Phe Thr	
580 585 590	
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Pro Thr Arg Phe Val Gln Phe Tyr Ala Asp Leu Glu Lys Ile Asn Gln	
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Ile Glu Tyr Thr Ser Asp Glu Lys Pro Tyr Ser Met Asp Ser Leu Thr	
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gta gga agt tat ttg gat ctt gca ggc aga tta tac gaa aac aaa cct	1968
Val Gly Ser Tyr Leu Asp Leu Ala Gly Arg Leu Tyr Glu Asn Lys Pro	
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 <213> Saccharomyces cerevisiae

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 35 40 45
 Ser Lys Phe Leu Asp Asp Arg Gly Asp Asn Glu Ser Leu Gln Leu Leu
 50 55 60
 Asn Asp Ile Glu Phe Thr Arg Leu Gly Leu Thr Pro Arg Glu Pro Val
 65 70 75 80
 Ile Ile Lys Asp Val Lys Thr Gly Lys Glu Arg Lys Leu His Gly Arg
 85 90 95
 Phe Leu His Ile Thr Asp Ile His Pro Asp Pro Tyr Tyr Val Glu Gly
 100 105 110

Sequence Listing PCT-JP03-00117.txt

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115 120 125
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145 150 155 160
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165 170 175
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180 185 190
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195 200 205
Glu Asp Pro Arg Asp Phe Asp Val Ser Val Ile Pro Ser Leu Gly Asn
210 215 220
Asn Asp Val Phe Pro His Asn Met Phe Ala Leu Gly Pro Thr Leu Gln
225 230 235 240
Thr Arg Glu Tyr Tyr Arg Ile Trp Lys Asn Phe Val Pro Gln Gln Gln
245 250 255
Gln Arg Thr Phe Asp Arg Ser Ala Ser Phe Leu Thr Glu Val Ile Pro
260 265 270
Gly Lys Leu Ala Val Leu Ser Ile Asn Thr Leu Tyr Leu Phe Lys Ala
275 280 285
Asn Pro Leu Val Asp Asn Cys Asn Ser Lys Lys Glu Pro Gly Tyr Gln
290 295 300
Leu Leu Leu Trp Phe Gly Tyr Val Leu Glu Glu Leu Arg Ser Arg Gly
305 310 315 320
Met Lys Val Trp Leu Ser Gly His Val Pro Pro Ile Ala Lys Asn Phe
325 330 335
Asp Gln Ser Cys Tyr Asp Lys Phe Thr Leu Trp Thr His Glu Tyr Arg
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355 360 365
Ile Pro Thr Asp Gly Lys Lys Ala Arg Lys Ser Leu Leu Lys Ala Met
370 375 380
Glu Gln Ser Thr Arg Val Gln Gln Gly Glu Asp Ser Asn Glu Glu Asp
385 390 395 400
Glu Glu Thr Glu Leu Asn Arg Ile Leu Asp His Ala Met Ala Ala Lys
405 410 415
Glu Val Phe Leu Met Gly Ala Lys Pro Ser Asn Lys Glu Ala Tyr Met
420 425 430
Asn Thr Val Arg Asp Thr Tyr Tyr Arg Lys Val Trp Asn Lys Leu Glu
435 440 445

Sequence Listing PCT-JP03-00117.txt

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Arg Tyr Ser Ile Val Asn Ile Gly Gly Ser Val Ile Pro Thr Phe Asn
 485 490 495

Pro Ser Phe Arg Ile Trp Glu Tyr Asn Ile Thr Asp Ile Val Asn Asp
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Ser Asn Phe Ala Val Ser Glu Tyr Lys Pro Trp Asp Glu Phe Phe Glu
 515 520 525

Ser Leu Asn Lys Ile Met Glu Asp Ser Leu Leu Glu Asp Glu Met Asp
 530 535 540

Ser Ser Asn Ile Glu Val Gly Ile Asn Arg Glu Lys Met Gly Glu Lys
 545 550 555 560

Lys Asn Lys Lys Lys Lys Lys Asn Asp Lys Thr Met Pro Ile Glu Met
 565 570 575

Pro Asp Lys Tyr Glu Leu Gly Pro Ala Tyr Val Pro Gln Leu Phe Thr
 580 585 590

Pro Thr Arg Phe Val Gln Phe Tyr Ala Asp Leu Glu Lys Ile Asn Gln
 595 600 605

Glu Leu His Asn Ser Phe Val Glu Ser Lys Asp Ile Phe Arg Tyr Glu
 610 615 620

Ile Glu Tyr Thr Ser Asp Glu Lys Pro Tyr Ser Met Asp Ser Leu Thr
 625 630 635 640

Val Gly Ser Tyr Leu Asp Leu Ala Gly Arg Leu Tyr Glu Asn Lys Pro
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Asp Asp

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 <211> 405
 <212> DNA
 <213> Rattus rattus

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 Page 24

Sequence Listing PCT-JP03-00117.txt

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      35      40      45
gaa gtc cta aga gag caa gct ggg ggt gat gct act gag aac ttt gag 192
Glu Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu
      50      55      60
gac gtc ggg cac tct acg gat gca cga gaa ctg tcc aaa aca tac atc 240
Asp Val Gly His Ser Thr Asp Ala Arg Glu Leu Ser Lys Thr Tyr Ile
      65      70      75      80
atc ggg gag ctg cat cca gat gac aga tca aag ata gcc aag cct tcg 288
Ile Gly Glu Leu His Pro Asp Asp Arg Ser Lys Ile Ala Lys Pro Ser
      85      90      95
gaa acc ctt atc act act gtc gag tct aat tcc agt tgg tgg acc aac 336
Glu Thr Leu Ile Thr Thr Val Glu Ser Asn Ser Ser Trp Trp Thr Asn
      100      105      110
tgg gtg atc cca gcc atc tca gcc ctg gtg gta gct ctg atg tat cgc 384
Trp Val Ile Pro Ala Ile Ser Ala Leu Val Val Ala Leu Met Tyr Arg
      115      120      125
ctc tac atg gca gaa gat taa 405
Leu Tyr Met Ala Glu Asp
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<211> 134
<212> PRT
<213> Rattus rattus

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      35      40      45
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      50      55      60
Asp Val Gly His Ser Thr Asp Ala Arg Glu Leu Ser Lys Thr Tyr Ile
      65      70      75      80
Ile Gly Glu Leu His Pro Asp Asp Arg Ser Lys Ile Ala Lys Pro Ser
      85      90      95
Glu Thr Leu Ile Thr Thr Val Glu Ser Asn Ser Ser Trp Trp Thr Asn
      100      105      110
Trp Val Ile Pro Ala Ile Ser Ala Leu Val Val Ala Leu Met Tyr Arg
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Sequence Listing PCT-JP03-00117.txt

130

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 <211> 363
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 Phe Lys Asp Glu His Pro Gly Gly Asp Glu Ile Ile Met Asp Leu Gly
 35 40 45
 gga caa gat gct aca gaa agc ttt gtc gat atc ggt cat tct gac gaa 192
 Gly Gln Asp Ala Thr Glu Ser Phe Val Asp Ile Gly His Ser Asp Glu
 50 55 60
 gca ttg aga cta ctg aaa ggt tta tac att ggt gac gtt gac aag acc 240
 Ala Leu Arg Leu Leu Lys Gly Leu Tyr Ile Gly Asp Val Asp Lys Thr
 65 70 75
 agt gag cgc gtt tct gtg gaa aag gta tct acc tct gaa aac caa agt 288
 Ser Glu Arg Val Ser Val Glu Lys Val Ser Thr Ser Glu Asn Gln Ser
 85 90 95
 aaa ggt agt ggt aca ttg gtt gtc ata ttg gcc att tta atg cta ggt 336
 Lys Gly Ser Gly Thr Leu Val Val Ile Leu Ala Ile Leu Met Leu Gly
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 gtt gct tat tat ttg ttg aac gaa taa 363
 Val Ala Tyr Tyr Leu Leu Asn Glu
 115 120

<210> 14
 <211> 120
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 35 40 45
 Gly Gln Asp Ala Thr Glu Ser Phe Val Asp Ile Gly His Ser Asp Glu

Sequence Listing PCT-JP03-00117.txt

50

55

60

Ala Leu Arg Leu Leu Lys Gly Leu Tyr Ile Gly Asp Val Asp Lys Thr
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85 90 95
Lys Gly Ser Gly Thr Leu Val Val Ile Leu Ala Ile Leu Met Leu Gly
100 105 110
Val Ala Tyr Tyr Leu Leu Asn Glu
115 120